

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/591,576
Source: IFWP
Date Processed by STIC: 9/15/06

ENTERED



IFWP

RAW SEQUENCE LISTING

DATE: 09/15/2006

PATENT APPLICATION: US/10/591,576

TIME: 09:13:59

Input Set : A:\SHIMIZU-13111_sq.txt

Output Set: N:\CRF4\09152006\J591576.raw

3 <110> APPLICANT: KAKU, Hanae
 4 SHIBUYA, Naoto
 5 MINAMI, Eiichi
 6 MINAMI, Naoko
 7 NISHIZAWA, Yoko
 8 TAKIO, Koji
 9 DOHMAE, Naoshi
 11 <120> TITLE OF INVENTION: CHITIN OLIGOSACCHARIDE ELICITOR-BINDING PROTEINS
 13 <130> FILE REFERENCE: SHIMIZU-13111
 C--> 15 <140> CURRENT APPLICATION NUMBER: US/10/591,576
 C--> 15 <141> CURRENT FILING DATE: 2006-08-31
 15 <150> PRIOR APPLICATION NUMBER: PCT/JP2005/003451
 16 <151> PRIOR FILING DATE: 2005-03-02
 18 <150> PRIOR APPLICATION NUMBER: JP2004-59551
 19 <151> PRIOR FILING DATE: 2004-03-03
 21 <160> NUMBER OF SEQ ID NOS: 23
 23 <170> SOFTWARE: PatentIn version 3.3
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 1071
 27 <212> TYPE: DNA
 28 <213> ORGANISM: Oryza sativa
 31 <220> FEATURE:
 32 <221> NAME/KEY: CDS
 33 <222> LOCATION: (1)..(1071)
 35 <400> SEQUENCE: 1
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 37 Met Ala Ser Leu Thr Ala Ala Leu Ala Thr Pro Ala Ala Ala Ala Leu
 38 1 5 10 15
 40 ctc ctc ctc gtc ctc ctc gcc gcc ccc gcc tcc gcc gcc aac ttc acc 96
 41 Leu Leu Leu Val Leu Leu Ala Ala Pro Ala Ser Ala Ala Asn Phe Thr
 42 20 25 30
 44 tgc gcg gtg gct tca ggc acc acc tgc aag tcc gcc atc ctc tac acc 144
 45 Cys Ala Val Ala Ser Gly Thr Thr Cys Lys Ser Ala Ile Leu Tyr Thr
 46 35 40 45
 48 tcc ccc aac gcc acc acc tac ggc aac ctc gtc gcc cgc ttc aac acc 192
 49 Ser Pro Asn Ala Thr Thr Tyr Gly Asn Leu Val Ala Arg Phe Asn Thr
 50 50 55 60
 52 acc acc ctc ccc gac ctc ctc ggc gcc aac ggc ctc ccc gac ggc acg 240
 53 Thr Thr Leu Pro Asp Leu Leu Gly Ala Asn Gly Leu Pro Asp Gly Thr
 54 65 70 75 80
 56 ctt tcc tcc gcc ccc gtc gcc gcc aat tcc acc gtc aaa atc ccc ttc 288
 57 Leu Ser Ser Ala Pro Val Ala Ala Asn Ser Thr Val Lys Ile Pro Phe
 58 85 90 95

see
p. 6

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60 cgc tgc cgc tgc aac ggc gac gtc ggc cag tcg gac cgc ctc ccc atc      336
61 Arg Cys Arg Cys Asn Gly Asp Val Gly Gln Ser Asp Arg Leu Pro Ile
62          100          105          110
64 tac gtc gtg cag ccg cag gac ggg ctc gac gcc atc gcg cgc aac gtg      384
65 Tyr Val Val Gln Pro Gln Asp Gly Leu Asp Ala Ile Ala Arg Asn Val
66          115          120          125
68 ttc aac gcc ttc gtc acc tac cag gag atc gcc gcc gcg aac aac atc      432
69 Phe Asn Ala Phe Val Thr Tyr Gln Glu Ile Ala Ala Asn Asn Ile
70          130          135          140
72 ccc gac ccc aac aag ata aat gtc agc cag acg ctg tgg att ccg ctg      480
73 Pro Asp Pro Asn Lys Ile Asn Val Ser Gln Thr Leu Trp Ile Pro Leu
74 145          150          155          160
76 ccc tgc agc tgc gac aag gag gaa ggc tct aac gtg atg cac ctc gcc      528
77 Pro Cys Ser Cys Asp Lys Glu Glu Gly Ser Asn Val Met His Leu Ala
78          165          170          175
80 tac agc gtc ggc aaa ggg gag aac acg tcg gcg atc gct gcc aag tac      576
81 Tyr Ser Val Gly Lys Gly Glu Asn Thr Ser Ala Ile Ala Ala Lys Tyr
82          180          185          190
84 ggg gtg acg gag tcc acg ctt ctc acc aga aat aag atc gac gac ccc      624
85 Gly Val Thr Glu Ser Thr Leu Leu Thr Arg Asn Lys Ile Asp Asp Pro
86          195          200          205
88 acg aaa ttg cag atg gga cag att cta gat gtc ccg ctc cct gtg tgc      672
89 Thr Lys Leu Gln Met Gly Gln Ile Leu Asp Val Pro Leu Pro Val Cys
90          210          215          220
92 cgt tca tca atc agc gat acc tca gct gat cac aat ctg atg ctc ctc      720
93 Arg Ser Ser Ile Ser Asp Thr Ser Ala Asp His Asn Leu Met Leu Leu
94 225          230          235          240
96 ccg gat ggc acc tat gga ttc acc gca gga aac tgc atc cgc tgc agc      768
97 Pro Asp Gly Thr Tyr Gly Phe Thr Ala Gly Asn Cys Ile Arg Cys Ser
98          245          250          255
100 tgc agt tca act acc tac cag cta aac tgc act gca gta cag aac aag      816
101 Cys Ser Ser Thr Thr Tyr Gln Leu Asn Cys Thr Ala Val Gln Asn Lys
102          260          265          270
104 gga tgc ccg tca gtg cca ctg tgc aat gga acg ctg aag ctt ggt gag      864
105 Gly Cys Pro Ser Val Pro Leu Cys Asn Gly Thr Leu Lys Leu Gly Glu
106          275          280          285
108 acg aac ggc acc ggt tgc gga tca aca acg tgc gcc tac agt ggt tac      912
109 Thr Asn Gly Thr Gly Cys Gly Ser Thr Thr Cys Ala Tyr Ser Gly Tyr
110          290          295          300
112 tcc aac agt tca tcg ctc atc ata caa acc agc ctt gca act aat cag      960
113 Ser Asn Ser Ser Ser Leu Ile Ile Gln Thr Ser Leu Ala Thr Asn Gln
114 305          310          315          320
116 aca aca gcc tgc cag aga gga gga tct ggg agg tcg cag ttc gct agg      1008
117 Thr Thr Ala Cys Gln Arg Gly Gly Ser Gly Arg Ser Gln Phe Ala Arg
118          325          330          335
120 tcc atg tgg agc atg tct gtt atc tcc ttc cac atg gtg ttg atc att      1056
121 Ser Met Trp Ser Met Ser Val Ile Ser Phe His Met Val Leu Ile Ile
122          340          345          350
124 atc tgt ttc ctt tga      1071

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125 Ile Cys Phe Leu
126          355
129 <210> SEQ ID NO: 2
130 <211> LENGTH: 356
131 <212> TYPE: PRT
132 <213> ORGANISM: Oryza sativa
134 <400> SEQUENCE: 2
136 Met Ala Ser Leu Thr Ala Ala Leu Ala Thr Pro Ala Ala Ala Leu
137 1          5          10          15
140 Leu Leu Leu Val Leu Leu Ala Ala Pro Ala Ser Ala Ala Asn Phe Thr
141          20          25          30
144 Cys Ala Val Ala Ser Gly Thr Thr Cys Lys Ser Ala Ile Leu Tyr Thr
145          35          40          45
148 Ser Pro Asn Ala Thr Thr Tyr Gly Asn Leu Val Ala Arg Phe Asn Thr
149          50          55          60
152 Thr Thr Leu Pro Asp Leu Leu Gly Ala Asn Gly Leu Pro Asp Gly Thr
153 65          70          75          80
156 Leu Ser Ser Ala Pro Val Ala Ala Asn Ser Thr Val Lys Ile Pro Phe
157          85          90          95
160 Arg Cys Arg Cys Asn Gly Asp Val Gly Gln Ser Asp Arg Leu Pro Ile
161          100         105         110
164 Tyr Val Val Gln Pro Gln Asp Gly Leu Asp Ala Ile Ala Arg Asn Val
165          115         120         125
168 Phe Asn Ala Phe Val Thr Tyr Gln Glu Ile Ala Ala Asn Asn Ile
169          130         135         140
172 Pro Asp Pro Asn Lys Ile Asn Val Ser Gln Thr Leu Trp Ile Pro Leu
173 145         150         155         160
176 Pro Cys Ser Cys Asp Lys Glu Glu Gly Ser Asn Val Met His Leu Ala
177          165         170         175
180 Tyr Ser Val Gly Lys Gly Glu Asn Thr Ser Ala Ile Ala Ala Lys Tyr
181          180         185         190
184 Gly Val Thr Glu Ser Thr Leu Leu Thr Arg Asn Lys Ile Asp Asp Pro
185          195         200         205
188 Thr Lys Leu Gln Met Gly Gln Ile Leu Asp Val Pro Leu Pro Val Cys
189          210         215         220
192 Arg Ser Ser Ile Ser Asp Thr Ser Ala Asp His Asn Leu Met Leu Leu
193 225         230         235         240
196 Pro Asp Gly Thr Tyr Gly Phe Thr Ala Gly Asn Cys Ile Arg Cys Ser
197          245         250         255
200 Cys Ser Ser Thr Tyr Gln Leu Asn Cys Thr Ala Val Gln Asn Lys
201          260         265         270
204 Gly Cys Pro Ser Val Pro Leu Cys Asn Gly Thr Leu Lys Leu Gly Glu
205          275         280         285
208 Thr Asn Gly Thr Gly Cys Gly Ser Thr Thr Cys Ala Tyr Ser Gly Tyr
209          290         295         300
212 Ser Asn Ser Ser Ser Leu Ile Ile Gln Thr Ser Leu Ala Thr Asn Gln
213 305         310         315         320
216 Thr Thr Ala Cys Gln Arg Gly Gly Ser Gly Arg Ser Gln Phe Ala Arg
217          325         330         335

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220 Ser Met Trp Ser Met Ser Val Ile Ser Phe His Met Val Leu Ile Ile
221          340          345          350
224 Ile Cys Phe Leu
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229 <211> LENGTH: 987
230 <212> TYPE: DNA
231 <213> ORGANISM: Oryza sativa
234 <220> FEATURE:
235 <221> NAME/KEY: CDS
236 <222> LOCATION: (1)..(987)
238 <400> SEQUENCE: 3
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240 Ala Asn Phe Thr Cys Ala Val Ala Ser Gly Thr Thr Cys Lys Ser Ala
241 1          5          10          15
243 atc ctc tac acc tcc ccc aac gcc acc acc tac ggc aac ctc gtc gcc      96
244 Ile Leu Tyr Thr Ser Pro Asn Ala Thr Thr Tyr Gly Asn Leu Val Ala
245          20          25          30
247 cgc ttc aac acc acc acc ctc ccc gac ctc ctc ggc gcc aac ggc ctc     144
248 Arg Phe Asn Thr Thr Thr Leu Pro Asp Leu Leu Gly Ala Asn Gly Leu
249          35          40          45
251 ccc gac ggc acg ctt tcc tcc gcc ccc gtc gcc gcc aat tcc acc gtc     192
252 Pro Asp Gly Thr Leu Ser Ser Ala Pro Val Ala Ala Asn Ser Thr Val
253          50          55          60
255 aaa atc ccc ttc cgc tgc cgc tgc aac ggc gac gtc ggc cag tcg gac     240
256 Lys Ile Pro Phe Arg Cys Arg Cys Asn Gly Asp Val Gly Gln Ser Asp
257 65          70          75          80
259 cgc ctc ccc atc tac gtc gtg cag ccg cag gac ggg ctc gac gcc atc     288
260 Arg Leu Pro Ile Tyr Val Val Gln Pro Gln Asp Gly Leu Asp Ala Ile
261          85          90          95
263 gcg cgc aac gtg ttc aac gcc ttc gtc acc tac cag gag atc gcc gcc     336
264 Ala Arg Asn Val Phe Asn Ala Phe Val Thr Tyr Gln Glu Ile Ala Ala
265          100          105          110
267 gcg aac aac atc ccc gac ccc aac aag ata aat gtc agc cag acg ctg     384
268 Ala Asn Asn Ile Pro Asp Pro Asn Lys Ile Asn Val Ser Gln Thr Leu
269          115          120          125
271 tgg att ccg ctg ccc tgc agc tgc gac aag gag gaa ggc tct aac gtg     432
272 Trp Ile Pro Leu Pro Cys Ser Cys Asp Lys Glu Glu Gly Ser Asn Val
273          130          135          140
275 atg cac ctc gcc tac agc gtc ggc aaa ggg gag aac acg tcg gcg atc     480
276 Met His Leu Ala Tyr Ser Val Gly Lys Gly Glu Asn Thr Ser Ala Ile
277 145          150          155          160
279 gct gcc aag tac ggg gtg acg gag tcc acg ctt ctc acc aga aat aag     528
280 Ala Ala Lys Tyr Gly Val Thr Glu Ser Thr Leu Leu Thr Arg Asn Lys
281          165          170          175
283 atc gac gac ccc acg aaa ttg cag atg gga cag att cta gat gtc ccg     576
284 Ile Asp Asp Pro Thr Lys Leu Gln Met Gly Gln Ile Leu Asp Val Pro
285          180          185          190
287 ctc cct gtg tgc cgt tca tca atc agc gat acc tca gct gat cac aat     624

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288 Leu Pro Val Cys Arg Ser Ser Ile Ser Asp Thr Ser Ala Asp His Asn
289      195      200      205
291 ctg atg ctc ctc ccg gat ggc acc tat gga ttc acc gca gga aac tgc      672
292 Leu Met Leu Leu Pro Asp Gly Thr Tyr Gly Phe Thr Ala Gly Asn Cys
293      210      215      220
295 atc cgc tgc agc tgc agt tca act acc tac cag cta aac tgc act gca      720
296 Ile Arg Cys Ser Cys Ser Ser Thr Thr Tyr Gln Leu Asn Cys Thr Ala
297 225      230      235      240
299 gta cag aac aag gga tgc ccg tca gtg cca ctg tgc aat gga acg ctg      768
300 Val Gln Asn Lys Gly Cys Pro Ser Val Leu Cys Asn Gly Thr Leu
301      245      250      255
303 aag ctt ggt gag acg aac ggc acc ggt tgc gga tca aca acg tgc gcc      816
304 Lys Leu Gly Glu Thr Asn Gly Thr Gly Cys Gly Ser Thr Thr Cys Ala
305      260      265      270
307 tac agt ggt tac tcc aac agt tca tgc ctc atc ata caa acc agc ctt      864
308 Tyr Ser Gly Tyr Ser Asn Ser Ser Ser Leu Ile Ile Gln Thr Ser Leu
309      275      280      285
311 gca act aat cag aca aca gcc tgc cag aga gga gga tct ggg agg tgc      912
312 Ala Thr Asn Gln Thr Thr Ala Cys Gln Arg Gly Gly Ser Gly Arg Ser
313      290      295      300
315 cag ttc gct agg tcc atg tgg agc atg tct gtt atc tcc ttc cac atg      960
316 Gln Phe Ala Arg Ser Met Trp Ser Met Ser Val Ile Ser Phe His Met
317 305      310      315      320
319 gtg ttg atc att atc tgt ttc ctt tga      987
320 Val Leu Ile Ile Ile Cys Phe Leu
321      325
324 <210> SEQ ID NO: 4
325 <211> LENGTH: 328
326 <212> TYPE: PRT
327 <213> ORGANISM: Oryza sativa
329 <400> SEQUENCE: 4
331 Ala Asn Phe Thr Cys Ala Val Ala Ser Gly Thr Thr Cys Lys Ser Ala
332 1      5      10      15
335 Ile Leu Tyr Thr Ser Pro Asn Ala Thr Thr Tyr Gly Asn Leu Val Ala
336      20      25      30
339 Arg Phe Asn Thr Thr Thr Leu Pro Asp Leu Leu Gly Ala Asn Gly Leu
340      35      40      45
343 Pro Asp Gly Thr Leu Ser Ser Ala Pro Val Ala Ala Asn Ser Thr Val
344      50      55      60
347 Lys Ile Pro Phe Arg Cys Arg Cys Asn Gly Asp Val Gly Gln Ser Asp
348 65      70      75      80
351 Arg Leu Pro Ile Tyr Val Val Gln Pro Gln Asp Gly Leu Asp Ala Ile
352      85      90      95
355 Ala Arg Asn Val Phe Asn Ala Phe Val Thr Tyr Gln Glu Ile Ala Ala
356      100      105      110
359 Ala Asn Asn Ile Pro Asp Pro Asn Lys Ile Asn Val Ser Gln Thr Leu
360      115      120      125
363 Trp Ile Pro Leu Pro Cys Ser Cys Asp Lys Glu Glu Gly Ser Asn Val
364      130      135      140

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/591,576

DATE: 09/15/2006
TIME: 09:14:00

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:9; Xaa Pos. 2,5,13,30

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:11,12,14,15,16,17,18,19,20,21,22,23

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/591,576

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Input Set : A:\SHIMIZU-13111_sq.txt

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L:15 M:270 C: Current Application Number differs, Replaced Current Application No

L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:802 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0

M:341 Repeated in SeqNo=9